



## Blast 2 Sequences results

## PubMed

**Entrez**

# BLAST

OMIM

## Taxonomy

## Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]**

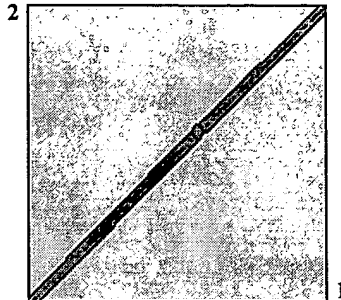
Match:  Mismatch:  gap open:  gap extension:

x\_dropoff:  expect:  wordsize:  Filter ☒

## Align

**Sequence 1** lcl|seq\_1 **Length** 2268 (1 .. 2268)

**Sequence 2** |cl|seq\_2 Length 2268 (1 .. 2268)



**NOTE:**The statistics (bitscore and expect value) is calculated based on the size of nr database

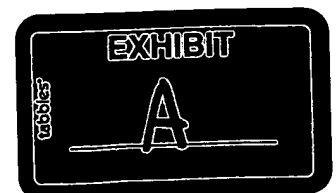
**NOTE:**If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3603 bits (1874), Expect = 0.0  
Identities = 2140/2268 (94%), Gaps = 2/2268 (0%)  
Strand = Plus / Plus

Query:	1	atgtcagcttcacctctccttgataaccagtgcgatcatctcccaaccaaagtgtggat	60
Sbjct:	1	atgtcagcttcagctctccttgataaccagtgcgatcattctctaccaaagtgtggat	60
Query:	61	ctgacaatggtcgataaggcggatgaattggaccgcagggtttccgatgccttcttagaa	120
Sbjct:	61	ctgataatggtcgataaggctgatgaattggaccgcagggtttccgatgccttctcagaa	120
Query:	121	cgagaagcttctaggggaaggaggattactcaaagctccaccgatgacgcgctgggtta	180
Sbjct:	121	cgtgaagcttctaggggaaggatgattactcaaattctccggcgagtgcagcgctgggtta	180
Query:	181	gcttgcaaaaaggctggccgatggctcgcttccccgagatctcagctggttgaaaggtagca	240
Sbjct:	181	gcttgcaaaaaggctggccgacggtcgcttccccgagatctcagctggttgagaaggtagca	240
Query:	241	gttctctccgcttatatctatattggcaagaaattctggggcggatacttgaatcgaaa	300
Sbjct:	241	gccctctccgcttacatctatgttgcaaggaaattctggggcggatacttgaatcgaaa	300
Query:	301	ccttgggcgcgggcaacagtgagtggtctcgttgccatcgacttggacaccatttgcattg	360
Sbjct:	301	ccttgggcgcgagcaagagtgcagtggtctcgttgccatcgaccttgcaccatttgcattg	360

SEB SA NO: 10 (octopne-type Ti)  
napoline-type Ti

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?>



Query: 361 gattttctccgaagcacaactaatccaagccctgtttttgctgagcggtaaaagatgtgca 420  
|||||  
Sbjct: 361 gattttctccgaagcacaacttctccaaaccctgtttttgctgagcggtaaaagatgtgca 420

Query: 421 ccgattgatcttagtcatttcgtggccatttcaatctctaagactgccggctttcgaacc 480  
|||  
Sbjct: 421 tccagcgatcttagtcatttcgtggccatttcaatctctaagactgcccgctcccgaacc 480

Query: 481 ctgccaatgccgctgtacgagaatggcacgatgaaatgcgttacccgggtttaccataacc 540  
|||||  
Sbjct: 481 ctgcaaatgccgccttacgagaaaggcacgacgaaacgcgttacccgggtttaccctgacc 540

Query: 541 cttgaagggggccgtgccatttgacatggtagcttatggtcgaaacctgatgctgaagggt 600  
|||||  
Sbjct: 541 cttgaagaggccgtaccatttgacatggtagcttatggtcgaaacctgatgctgaagggt 600

Query: 601 tcggcagggttcctttccaacaatcgacttgctctacgactgcagaccgttttttgacaa 660  
|||||  
Sbjct: 601 tcggcagggttcctttccaacaattgacttgctctatgactacagatcgtttttgacaa 660

Query: 661 tgttccgatagtgacggatcggtctcttccggaggatgttcctaagccgaaagtggcg 720  
|||||  
Sbjct: 661 tgttccgatagtgacggatcggtctcttccggaaagtgttcctaagccaaaagtggcg 720

Query: 721 gtcattggcgctggcatttccggactcgtggtggcaaacgaactgcttcacatgctgggta 780  
|||||  
Sbjct: 721 atcattggcgctggcatttccggactcgtggtggcaagcgaactgcttcacatgctgggta 780

Query: 781 gacgatgttacaatatatgaagcaagtgatcggttgaggcaagctttggtcacatgct 840  
|||||  
Sbjct: 781 gacgatgttacaatatatgaagcaagtgatcggttgaggcaagctttggtcacatgct 840

Query: 841 ttcagggacgctcctagtgtcgtggccgaaatggggcgatgcgatttcctcctgctgca 900  
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Sbjct: 841 ttcaaggacgctcccagcgtggtggccgaaatggggcgatgcgatttcctcctgctgca 900

Query: 901 ttctgctgtttttcttctcctcgagcgttacggcctgtcttcgatgaggccgttcccaat 960  
|||  
Sbjct: 901 tcgtgctgtttttcttctcctcgagcgttacggcctgtcttcgatgaggccgttcccaat 960

Query: 961 cccggcacagtcgacacttacttggctctaccaaggcgtccaatacatgtggaaagccggg 1020  
|||||  
Sbjct: 961 cccggcacagtcgacactaacttggctctaccaaggcctccgatacatgtggaaagccggg 1020

Query: 1021 cagctgccaccgaagctgttccatcgctttacaacgggtggcgctgcttctgaaggac 1080  
|||||  
Sbjct: 1021 cagcagccaccgaagctgttccatcgctttacagcgggtggcgctgcttctgaaggac 1080

Query: 1081 ggttttcatgagcgagatattgtgttggttcgcctgtcgtattactcaggccttgaaa 1140  
|||||  
Sbjct: 1081 ggtttccatgagggagatattgtgttggttcgcctgttctattactcaagccttgaaa 1140

Query: 1141 tcaggacacattaggtgggctcatgactcctggcaaatgttgctgaaccgtttcgggagg 1200  
|||||  
Sbjct: 1141 tcaggagacattagggggctcatgactcctggcaaatgttgctgaaccgtttcgggagg 1200

Query: 1201 gagtccttctcttcagggatagagaggatcttctgggcacacatcctcctggtggt-aa 1259  
|||||  
Sbjct: 1201 gagtccttctcttcagcgatagagaggatcttctgggcacacatcctcctggtggtgaa 1260

Query: 1260 acatggagttttcctcatgattgggacattcaagctaattgggaataggatctggcggg 1319  
|||||  
Sbjct: 1261 acatggagtttccctcatgattgggacattcaagctaattgggaataggatctggc-gg 1319

Query: 1320 gtttggtccagtttttgaaagcgggtttattgagatcctccgcttggtcatcaacggata 1379  
|||||  
Sbjct: 1320 gtttggtccagtttttgaaagcgggtttattgagatccttcgcttggtcataaacggata 1379

Query: 1380 tgaagaaaatcagcggatgtgccctgaaggaatctcagaacttcacgtcggatcgcatc 1439  
|||||  
Sbjct: 1380 tgaagaaaatcagcggatgtgctctgaaggaatctcagaacttcacgtcgaatagccac 1439

Query: 1440 tgaagtggttaacggtgtgtctgtgagccagcgcataatgccatgttcaagtcaggggcat 1499  
|||||  
Sbjct: 1440 tcaagtggttaacggtgtgtctgtgaagccagcgtatacgccatgttcaagtcaggggcat 1499

Query: 1500 tcagaaggaaaagacaaaaataagataaggcttaagagcgggatatctgaactttatga 1559  
| ||||  
Sbjct: 1500 tgagaaagaaaagacaaaaataagataaggcttaagagcgggatatctgaactttatga 1559

Query: 1560 taagtggtggtgcacatctggactcgcaaatatccaactcaggcattgcctgacatgcga 1619  
|||||  
Sbjct: 1560 taagtggtggtgtacatctggactcgcaaatatccaactcaggcattgtctgacatgcga 1619

Query: 1620 taccaatatctttcaggcaccagtgaaccaagcgggttgataacagccatatgacaggatc 1679  
|||||  
Sbjct: 1620 taccaccattttctgacagcgtgaaccaagcgggttgataacagccatatgacaggctc 1679

Query: 1680 gtcaaaactcttctctgatgactgaacgaaaattctggttagaccatatcctcccgtcttg 1739  
|||||  
Sbjct: 1680 gtcaaaactcttctctgatgactgaacgaaaattctggttagaccatatcctcccgtcctg 1739

Query: 1740 tgtcctcatggacgggatcgcaaaagcagtgattgcctggactatgagtcgcaggatcc 1799  
|||||  
Sbjct: 1740 tgtcctcatggacgggatcgcaaaagcagtgactgcctggactatgagccgcaggatcc 1799

Query: 1800 gaatggttaaaggctctagtgtcatcagttatacatgggaggacgactcccacaagctgtt 1859  
|||||  
Sbjct: 1800 gaatggttaaaggctctggtgtcatcagttatacatgggaggacgactcccacaagctgtt 1859

Query: 1860 ggcggtccccgacaaaaagagcgattatgtctgctgcgggacgcaatttcgagatcttt 1919  
|||||  
Sbjct: 1860 ggcggtccccgacaaaaagagcgattctgtctgctgcgggacgcaatttcgagatcttt 1919

Query: 1920 cccggcggtttgccagcacctatttcctgcctgcgctgattacgacaaaaatgttattca 1979  
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Sbjct: 1920 cccggcggtttgccagcatctagttcccgctgcgctgattacgacaaaaatgttattca 1979

Query: 1980 acatgattggcttacagacgagaatgccggggagctttcaaactcaaccggcggtgga 2039  
|||||  
Sbjct: 1980 acatgattggcttacagacgagaatgccggggagctttcaaactcaaccggcggtgga 2039

Query: 2040 ggatttttattctgaagaacttttcttcaagcactggacacggctaataatgataccggagt 2099  
|||||  
Sbjct: 2040 ggatttttattctgaagaacttttcttcaagcactggacatgactaatgataccggagt 2099

Query: 2100 ttacttggcgggttgagttgttccttcacaggtggatgggtggaggggtgctattcagac 2159  
|||||  
Sbjct: 2100 ttacttggcgggttgagttgttccttcaccgggtgatgggtggagggcgctattcagac 2159

Query: 2160 cgcgtgtaacgccgtctgtgcaattatccacaattgtggaggcattttggcaaagggcaa 2219  
|||||  
Sbjct: 2160 cgcgtgtaacgccgtctgtgcaattatccacaattgtggaggatattttggcaaagggcaa 2219

Query: 2220 tcctctcgaacactcttgggaagagatataactaccgcagtagaaaatta 2267  
|||||  
Sbjct: 2220 tcctctcgaacactcttgggaagagatataactaccgcaatagaaaatta 2267

CPU time: 0.09 user secs. 0.05 sys. secs 0.14 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 5  
Number of Sequences: 0  
Number of extensions: 5  
Number of successful extensions: 4  
Number of sequences better than 10.0: 1  
length of query: 2268  
length of database: 7,234,536,489  
effective HSP length: 25  
effective length of query: 2243  
effective length of database: 7,234,536,464  
effective search space: 16227065288752  
effective search space used: 16227065288752  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)